~~144.~~ 13 (Amended) The method according to claim ~~131~~, 1 wherein said probes have a combined complexity of between about 40 kb and 750 kb.

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~~145.~~ 14 (Amended) The method according to claim ~~144~~, 13 wherein said probes have a combined complexity of between about 50 kb and 400 kb.

~~150.~~ 19 (Amended) A method of staining target chromosomal DNA to detect in an interphase cell one or more genetic translocations identified with chromosomal abnormalities, said method comprising:

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(a) providing a heterogeneous mixture of two or more nucleic acid probes having a combined complexity of at least 40 kb, which probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that flank and/or extend partially or fully across breakpoint regions known to be associated with genetic translocations;

(b) reacting the heterogeneous mixture with the targeted chromosomal DNA by in situ hybridization;

(c) adding a distinct fluorescent label to each of said nucleic acid probes; and

(d) observing the proximity or overlap of the regions stained by each probe, to determine whether said translocation is present in the interphase cell.

Kindly add new claims 154-161 as follows:

--~~154~~ 23. The method according to claim ~~131~~ 1, wherein said probes have a combined complexity of between about 50 kb and 1 Mb.

155. A method of staining target chromosomal DNA to detect in an interphase cell one or more genetic translocations identified with chromosomal abnormalities, said method comprising:

(a) providing a heterogeneous mixture of two or more labeled nucleic acid probes having a combined complexity of at least 40 kb, which probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that flank and/or extend partially or fully across breakpoint regions known to be associated with genetic translocations;

(b) reacting the heterogeneous mixture with the targeted chromosomal DNA by in situ hybridization; and

(c) observing the proximity or overlap of the regions stained by each probe, to determine whether said translocation is present in the interphase cell.

156. The method according to claim 155, wherein said probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that flank breakpoint regions known to be associated with genetic translocations.

157. The method according to claim 155, wherein said probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that extend partially across breakpoint regions known to be associated with genetic translocations.